

ALIGNMENT OF CRY3 SEQUENCES

(Numbered according to Cry3BB)

(alpha helices underlined, beta sheets marked with + + +'s)

| | 1 | 10 | 20 | 30 | 40 |
|----------|--|-------------------------------------|-------------------|------------------|----------------------|
| CRY3C: | MNPNNRSEHDTIKATENNEVSNNHAQYPLADTP | - - | TLEELNY | | |
| CRY3BB2: | MNPNNRSEHDTIKVTPNSELPTNHNQYPLADNP | NPSTLEELNY | | | |
| CRY3BB: | MNPNNRSEHDTIKVTPNSELQTNHNQYPLADNP | NPSTLEELNY | | | |
| CRY3BA: | MIRMGGRKMNPNNRSEYDTIKVTPNSELPTNHNQYPLADNP | NPSTLEELNY | | | |
| CRY3A: | MIRKGGRKMNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLED | LN | | | |
| | 50 | 60 | 70 | 80 | 90 |
| CRY3C: | KEFLRRTTDNNVEALDSSTTKDAIQKGISIIGDLLGVVGF | FPYGGALVSFY | | | |
| CRY3BB2: | KEFLRMTEDSSTEVL | DNSTVKDAVGTGISVVGQILGVVGVPFAGALTSFY | | | |
| CRY3BB: | KEFLRMTEDSSTEVL | DNSTVKDAVGTGISVVGQILGVVGVPFAGALTSFY | | | |
| CRY3BA: | KEFLRMTADNSTEVL | DSSTVKDAVGTGISVVGQILGVVGVPFAGALTSFY | | | |
| CRY3A: | KEFLRMTADN | NTEALDSSTTKD | <u>VIQKGISVVG</u> | <u>DLLGVVGFP</u> | <u>FGGALVSFY</u> |
| | 100 | 110 | 120 | 130 | 140 |
| CRY3C: | TNLLNTIWPGE-DPLKAFMQQVEALIDQKIADYAKDKATAELQGLKNVFK | | | | |
| CRY3BB2: | QSFLDTIWPSDADPWKAFMAQVEVLIDKKIEEYAKSKALAE | LQGLQNNFE | | | |
| CRY3BB: | QSFLNTIWPSDADPWKAFMAQVEVLIDKKIEEYAKSKALAE | LQGLQNNFE | | | |
| CRY3BA: | QSFLNAIWPSDADPWKAFMAQVEVLIDKKIEEYAKSKALAE | LQGLQNNFE | | | |
| CRY3A: | <u>TNFLNTIWPSE-DPWKAFMEQVEALMDQKIADYAKN</u> | <u>KALAE</u> | <u>LQGLQNNVE</u> | | |
| | 150 | 160 | 170 | 180 | 190 |
| CRY3C: | DYVSALDSWDKTP | TLTRDGRSQGRI | RELF | SQAESHFR | SMPSFAVSGYEV |
| CRY3BB2: | DYVNALNSWKKTP | LSLRSKRSQDRI | RELF | SQAESHFR | NSMPSFAVSKFEV |
| CRY3BB: | DYVNALNSWKKTP | LSLRSKRSQDRI | RELF | SQAESHFR | NSMPSFAVSKFEV |
| CRY3BA: | DYVNALDSWKKAPV | NLSRRSQDRI | RELF | SQAESHFR | NSMPSFAVSKFEV |
| CRY3A: | <u>DYVSALSSWQKNPVSSRN</u> | <u>PHSQGRI</u> | <u>RELF</u> | <u>SQAESHFR</u> | <u>NSMPSFAISGYEV</u> |

FIG. 17A

Replacement Sheets

| | | | | | |
|----------|---|-----|-----|-----|-----|
| | 200 | 210 | 220 | 230 | 240 |
| CRY3C: | LFLPTYAQAANTHLLLLKDAQIYGTDWGYSTDDLNEFHTKQKDLTIEYTN | | | | |
| CRY3BB2: | LFLPTYAQAANTHLLLLKDAQVFGEWGYSSSEDVAEFYHRQLKLTQQYTD | | | | |
| CRY3BB: | LFLPTYAQAANTHLLLLKDAQVFGEWGYSSSEDVAEFYHRQLKLTQQYTD | | | | |
| CRY3BA: | LFLPTYAQAANTHLLLLKDAQVFGEWGYSSSEDIAEFYQRQLKLTQQYTD | | | | |
| CRY3A: | <u>LFLTTYAQAANTHFLLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYTD</u> | | | | |

| | | | | | |
|----------|--|-----|-----|-----|-----|
| | 250 | 260 | 270 | 280 | 290 |
| CRY3C: | HCAKWYKAGLDKLRGSTYE EWVKFNRYRREMTLTVLDLITLFPDYVRTY | | | | |
| CRY3BB2: | HCVNWYNVGLNGLRGSTYDAWVKFNRFREMTLTVLDLIVLFPFYDVRLY | | | | |
| CRY3BB: | HCVNWYNVGLNGLRGSTYDAWVKFNRFREMTLTVLDLIVLFPFYDIRLY | | | | |
| CRY3BA: | HCVNWYNVGLNSLRGSTYDAWVKFNRFREMTLTVLDLIVLFPFYDVRLY | | | | |
| CRY3A: | <u>HCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPDYVRTY</u> | | | | |

| | | | | | |
|----------|--|-----|-----|-----|------|
| | 300 | 310 | 320 | 330 | 340 |
| CRY3C: | TKGVKTELTRDVLTDPPIVAVNNMNGYGTTFSNIENYIRKPHLFDYLHAIQ | | | | |
| CRY3BB2: | SKGVKTELTRDIFTDPIFSLNTLQEYGPTFLSIENSIRKPHLFDYLGQIE | | | | |
| CRY3BB: | SKGVKTELTRDIFTDPIFSLNTLQEYGPTFLSIENSIRKPHLFDYLGQIE | | | | |
| CRY3BA: | SKGVKTELTRDIFTDPIFTLNALQEYGPTFSSIENSIRKPHLFDYLRGIE | | | | |
| CRY3A: | <u>PKEVKTELTRDVLTDPPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLRHIQ</u> | | | | |
| | +++++ | | | | ++++ |

| | | | | | |
|----------|--|-------|-------|-------|-----|
| | 350 | 360 | 370 | 380 | 390 |
| CRY3C: | FHSRLQPGYFGTDSFNYWSGNYVSTRSSIGSDEIIRSPFYGNKSTLDVQN | | | | |
| CRY3BB2: | FHTRLQPGYSGKDSFNYWSGNYVETRPSIGSSKITITSPFYGDKSTEPVQK | | | | |
| CRY3BB: | FHTRLQPGYFGKDSFNYWSGNYVETRPSIGSSKITITSPFYGDKSTEPVQK | | | | |
| CRY3BA: | FHTRLRPGYSGKDSFNYWSGNYVETRPSIGSNDTITSPFYGDKSIEPIQK | | | | |
| CRY3A: | <u>FHTRFQPGYGGNDSFNYWSGNYVSTRPSIGSNDIITSPFYGNKSSEP VQN</u> | | | | |
| | +++++ | +++++ | +++++ | +++++ | +++ |

| | | | | |
|----------|--|-------|------|-------|
| | 400 | 410 | 420 | 430 |
| CRY3C: | LEFNGEKVFRAVANGNLAVWPVGTGGTKIHSGVTKVQFSQYNDRKDEVRT | | | |
| CRY3BB2: | LSFDGQKVYRTIANTDVAAPNG----KIYFGVTKVDFSQYDDQKNETST | | | |
| CRY3BB: | LSFDGQKVYRTIANTDVAAPNG----KVYLGVTKVDFSQYDDQKNETST | | | |
| CRY3BA: | LSFDGQKVYRTIANTDIAAFPDG----KIYFGVTKVDFSQYDDQKNETST | | | |
| CRY3A: | <u>LEFNGEKVYRAVANTNLAVWPSA----VYSGVTKVEFSQYNDQTDEAST</u> | | | |
| | +++ | +++++ | ++++ | +++++ |

FIG. 17B

Replacement Sheets

| | | | | | |
|----------|---|---------|-----------------|------|---------|
| | 440 | 450 | 460 | 470 | 480 |
| CRY3C: | QTYDSKRNVGGIV-FDSIDQLPPITTTDESLEKAYSHQLNYSVRCFLLQGGR | | | | |
| CRY3BB2: | QTYDSKRNNGHVGAQDSIDQLPPETTDEPLEKAYSHQLNYAECFLMQDRR | | | | |
| CRY3BB: | QTYDSKRNNGHVSAQDSIDQLPPETTDEPLEKAYSHQLNYAECFLMQDRR | | | | |
| CRY3BA: | QTYDSKRYNGYLGAQDSIDQLPPETTDEPLEKAYSHQLNYAECFLMQDRR | | | | |
| CRY3A: | QTYDSKRNVGAVS-WDSIDQLPPETTDEPLEKGYSHQLNYSVMCFLMQGSR | | | | |
| | ++++ | +++++ | | | +++++++ |
| | | | | | |
| | 490 | 500 | 510 | 520 | 530 |
| CRY3C: | GIIPVFTWTHKSVDFYNTLDSEKITQIPFVKAFILVNSTSVVAGPGFTGG | | | | |
| CRY3BB2: | GTIPFFTWTWTHRSVDFFNTIDAELITQLPVVKAYALSSGASIIIEGPGFTGG | | | | |
| CRY3BB: | GTIPFFTWTWTHRSVDFFNTIDAELITQLPVVKAYALSSGASIIIEGPGFTGG | | | | |
| CRY3BA: | GTIPFFTWTWTHRSVDFFNTIDAELITQLPVVKAYALSSGASIIIEGPGFTGG | | | | |
| CRY3A: | GTIPVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGG | | | | |
| | +++++++ | +++++ | ++++ | | +++++++ |
| | | | | | |
| | 540 | 550 | 560 | 570 | 580 |
| CRY3C: | DII-KCT-NGSGLTLYVTPAPDLTYSKTYKIRIRYASTSQVRFGIDLGSY | | | | |
| CRY3BB2: | NLLFLKESSNSIAKFKVTL-NSAALLQRYRVRIRYASTTNLRLFVQNSNN | | | | |
| CRY3BB: | NLLFLKESSNSIAKFKVTL-NSAALLQRYRVRIRYASTTNLRLFVQNSNN | | | | |
| CRY3BA: | NLLFLKESSNSIAKFKVTL-NSAALLQRYRVRIRYASTTNLRLFVQNSNN | | | | |
| CRY3A: | DII-QCTENGAATIYVTPD--VSYSQKYRARIHYASTSQITFTLSLDGA | | | | |
| | ++++++ | +++++++ | +++++++ | | ++++++ |
| | | | | | |
| | 590 | 600 | 610 | 620 | 630 |
| CRY3C: | THSISYFDKTMKGNLTLYNSFNLSSVSRPIEISG-GNKIGVSVGGIGSG | | | | |
| CRY3BB2: | DFIVIYINKTMNIDDDLTYQTFDLATTNSNMGFSGDTNELIIGAESFVSN | | | | |
| CRY3BB: | DFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESFVSN | | | | |
| CRY3BA: | DFLVIYINKTMNIDGDLTYQTFDFATSNSNMGFSGDTNDFIIGAESFVSN | | | | |
| CRY3A: | PFNQYYFDKTINKGDTLYNSFNLASFSTPFELSG--NNLQIGVTGLSAG | | | | |
| | +++++++ | | +++++++ | ++++ | +++++++ |
| | | | | | |
| | 640 | 650 | | | |
| CRY3C: | DEVYIDKIEFIPMD | | (SEQ ID NO:109) | | |
| CRY3BB2: | EKIYIDKIEFIPVQL | | (SEQ ID NO:110) | | |
| CRY3BB: | EKIYIDKIEFIPVQL | | (SEQ ID NO:111) | | |
| CRY3BA: | EKIYIDKIEFIPVQ | | (SEQ ID NO:112) | | |
| CRY3A: | DKVYIDKIEFIPVN | | (SEQ ID NO:113) | | |
| | +++++++ | | | | |

FIG. 17C